SEQUENCE LISTING

<110> Goossens, Alain
Inze, Dirk

<120> THE USE OF GENES ENCODING MEMBRANE TRANSPORTER PUMPS TO STIMULATE THE PRODUCTION OF SECONDARY METABOLITES IN BIOLOGICAL CELLS

<130> DI/ABC/V082

<150> EP01201407.2
<151> 2001-04-18

<160> 15

<170> PatentIn version 3.1

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tgttgttcca ac atg gag cca tca gat tta agt aat ttc cga ggt cga agt 171
Met Glu Pro Ser Asp Leu Ser Asn Phe Arg Gly Arg Ser
1 5 10

atg aga gga agt atg aga gga agt gta agg gaa aat agt aac tca ata 219
Met Arg Gly Ser Met Arg Gly Ser Val Arg Glu Asn Ser Asn Ser Ile
15 20 25

tgg agg aac aat gga gtt gaa ata ttt tca aga tca act aga gat gaa 267
Trp Arg Asn Asn Gly Val Glu Ile Phe Ser Arg Ser Thr Arg Asp Glu
30 35 40 45

gat gat gaa gag gca tta aaa tgg gca gca ctt gag aaa tta cca aca 315
Asp Asp Glu Glu Ala Leu Lys Trp Ala Ala Leu Glu Lys Leu Pro Thr
50 55 60

tat gat aga tta aga aaa ggt ata ttg ttt gga tca caa ggt act ggt 363
Tyr Asp Arg Leu Arg Lys Gly Ile Leu Phe Gly Ser Gln Gly Thr Gly
65 70 75

gtt gct gaa gtt gat gta gat gat ctt ggt gtt caa caa agg aag aat 411
Val Ala Glu Val Asp Val Asp Asp Leu Gly Val Gln Gln Arg Lys Asn
80 85 90

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ttg ctt gac aga ctt gtt aaa att gct gaa gaa gat aat gag aag ttc      459
Leu Leu Asp Arg Leu Val Lys Ile Ala Glu Glu Asp Asn Glu Lys Phe
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ttg ttg aaa ctc aag aac agg att gac agg gtt ggg att gat ttt cca      507
Leu Leu Lys Leu Lys Asn Arg Ile Asp Arg Val Gly Ile Asp Phe Pro
110                 115                 120                 125

tct ata gaa gtg aga ttt gag cat ctg aat att gag gca gat gca tat      555
Ser Ile Glu Val Arg Phe Glu His Leu Asn Ile Glu Ala Asp Ala Tyr
                130                 135                 140

gtt ggt agc aga gct ttg cct aca ttt acc aac ttc att tct aac ttc      603
Val Gly Ser Arg Ala Leu Pro Thr Phe Thr Asn Phe Ile Ser Asn Phe
            145                 150                 155

att gag tcc ctg ctg gat tca ctt cac atc ctt cca tcg aaa aaa cgt      651
Ile Glu Ser Leu Leu Asp Ser Leu His Ile Leu Pro Ser Lys Lys Arg
        160                 165                 170

tca gtt aca att ctc aag gat gtt agt ggt atc gtc aag ccc tgt cga      699
Ser Val Thr Ile Leu Lys Asp Val Ser Gly Ile Val Lys Pro Cys Arg
    175                 180                 185

atg act ctg ctt tta gga cct cca ggt tct ggg aaa aca act ttg tta      747
Met Thr Leu Leu Leu Gly Pro Pro Gly Ser Gly Lys Thr Thr Leu Leu
190                 195                 200                 205

ctt gct ttg gct gga aaa ctt gat tct gct cta agg gtt acg ggg aag      795
Leu Ala Leu Ala Gly Lys Leu Asp Ser Ala Leu Arg Val Thr Gly Lys
                210                 215                 220

gtg acg tat aat gga cac gaa tta cat gaa ttt gtg cca caa aga act      843
Val Thr Tyr Asn Gly His Glu Leu His Glu Phe Val Pro Gln Arg Thr
            225                 230                 235

gcg gcc tat att agc cag cat gat ttg cat att gga gaa atg act gtc      891
Ala Ala Tyr Ile Ser Gln His Asp Leu His Ile Gly Glu Met Thr Val
        240                 245                 250

aga gaa act ttg gag ttc tct gca aga tgc caa gga gtt ggt tct cgt      939
Arg Glu Thr Leu Glu Phe Ser Ala Arg Cys Gln Gly Val Gly Ser Arg
    255                 260                 265

tac gaa atg ttg gcc gaa ctg tca aga aga gag aaa gcg gct aat atc      987
Tyr Glu Met Leu Ala Glu Leu Ser Arg Arg Glu Lys Ala Ala Asn Ile
270                 275                 280                 285

aaa cca gat gct gat att gac atg ttc atg aag gct gca tca act gaa     1035
Lys Pro Asp Ala Asp Ile Asp Met Phe Met Lys Ala Ala Ser Thr Glu
                290                 295                 300

ggg caa gaa gcc aaa gtg att act gat tat gtt ctt aag att ctg gga     1083
Gly Gln Glu Ala Lys Val Ile Thr Asp Tyr Val Leu Lys Ile Leu Gly
            305                 310                 315
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ctg gat att tgt gca gat act atg gtg gga gat caa atg ata agg ggt     1131
Leu Asp Ile Cys Ala Asp Thr Met Val Gly Asp Gln Met Ile Arg Gly
        320                 325                 330

att tca gga gga cag aag aag cgt gtc act act ggt gaa atg att gtc     1179
Ile Ser Gly Gly Gln Lys Lys Arg Val Thr Thr Gly Glu Met Ile Val
    335                 340                 345

gga ccg tct aaa gcc ctt ttc atg gat gaa att tca act gga ctt gac     1227
Gly Pro Ser Lys Ala Leu Phe Met Asp Glu Ile Ser Thr Gly Leu Asp
350                 355                 360                 365

agt tcc aca act tac tcc atc gtg aat tcc cta aag caa tct gtt caa     1275
Ser Ser Thr Thr Tyr Ser Ile Val Asn Ser Leu Lys Gln Ser Val Gln
                370                 375                 380

atc ttg aaa gga aca gct ctg att tct ctc ttg cag cct gcc ccc gag     1323
Ile Leu Lys Gly Thr Ala Leu Ile Ser Leu Leu Gln Pro Ala Pro Glu
            385                 390                 395

act tac aac ttg ttc gat gat att gtt ctg cta tca gat ggc tac att     1371
Thr Tyr Asn Leu Phe Asp Asp Ile Val Leu Leu Ser Asp Gly Tyr Ile
        400                 405                 410

gtt tat cag ggt cca cga gag gaa gtg ctc gat ttc ttt gaa tcc atg     1419
Val Tyr Gln Gly Pro Arg Glu Glu Val Leu Asp Phe Phe Glu Ser Met
    415                 420                 425

gga ttc aaa tgc ccc aac aga aaa ggc gtg gct gac ttc ttg caa gaa     1467
Gly Phe Lys Cys Pro Asn Arg Lys Gly Val Ala Asp Phe Leu Gln Glu
430                 435                 440                 445

gtt aca tct aag aag gat caa cag caa tat tgg gta aag agg gac gag     1515
Val Thr Ser Lys Lys Asp Gln Gln Gln Tyr Trp Val Lys Arg Asp Glu
                450                 455                 460

cct tat agg ttt att aca tca aaa gaa ttt gct gag gct tat caa tct     1563
Pro Tyr Arg Phe Ile Thr Ser Lys Glu Phe Ala Glu Ala Tyr Gln Ser
            465                 470                 475

ttc cat gtt ggg aga aaa gta agc gat gaa ctt aca acc gca ttt gac     1611
Phe His Val Gly Arg Lys Val Ser Asp Glu Leu Thr Thr Ala Phe Asp
        480                 485                 490

aag agc aaa agc cac cct gct gct ttg act act gaa aag tat ggt att     1659
Lys Ser Lys Ser His Pro Ala Ala Leu Thr Thr Glu Lys Tyr Gly Ile
    495                 500                 505

gga gtg aaa caa ctt ttg aag gtt tgc acg gaa aga gag ttc ctt cta     1707
Gly Val Lys Gln Leu Leu Lys Val Cys Thr Glu Arg Glu Phe Leu Leu
510                 515                 520                 525

atg cag agg aat tca ttt gtt tac atc ttc aaa ttc ttt cag ctt atg     1755
Met Gln Arg Asn Ser Phe Val Tyr Ile Phe Lys Phe Phe Gln Leu Met
                530                 535                 540
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gta att gca ctt atg aca atg acc ata ttt ttt cga act aag atg tct     1803
Val Ile Ala Leu Met Thr Met Thr Ile Phe Phe Arg Thr Lys Met Ser
            545                 550                 555

cgg gat act gag acc gat gga gga att tat tct ggt gct ctc ttt ttt     1851
Arg Asp Thr Glu Thr Asp Gly Gly Ile Tyr Ser Gly Ala Leu Phe Phe
        560                 565                 570

acg gtt gtt atg ctt atg ttt aat ggt ttg tct gag ctt cct ttg aca     1899
Thr Val Val Met Leu Met Phe Asn Gly Leu Ser Glu Leu Pro Leu Thr
    575                 580                 585

ctc tac aag ctc ccg gtc ttc tac aag caa agg gac ttt ctc ttc tat     1947
Leu Tyr Lys Leu Pro Val Phe Tyr Lys Gln Arg Asp Phe Leu Phe Tyr
590                 595                 600                 605

cct tca tgg gct tat gca gtt cct tca tgg atc cta aaa atc cct gta     1995
Pro Ser Trp Ala Tyr Ala Val Pro Ser Trp Ile Leu Lys Ile Pro Val
                610                 615                 620

act ttt ctt gaa gtt ggg atg tgg gtg ttt ctc acc tat tat gtc atc     2043
Thr Phe Leu Glu Val Gly Met Trp Val Phe Leu Thr Tyr Tyr Val Ile
            625                 630                 635

gga ttt gat cct aat gtt gga aga ttt ttc aaa caa ttt ttg cta ctc     2091
Gly Phe Asp Pro Asn Val Gly Arg Phe Phe Lys Gln Phe Leu Leu Leu
        640                 645                 650

ata gta gta aac cag atg gca tca gga ttg ttc agg ttt att gca gca     2139
Ile Val Val Asn Gln Met Ala Ser Gly Leu Phe Arg Phe Ile Ala Ala
    655                 660                 665

gtt gga agg acc atg gga gtt gct agc aca ttt gga gca ttt gcg ctg     2187
Val Gly Arg Thr Met Gly Val Ala Ser Thr Phe Gly Ala Phe Ala Leu
670                 675                 680                 685

ctt tta caa ttt gca ttg ggc ggt ttt gtc ctt gca cga act gac gtg     2235
Leu Leu Gln Phe Ala Leu Gly Gly Phe Val Leu Ala Arg Thr Asp Val
                690                 695                 700

aag gac tgg tgg att tgg gga tac tgg acc tca cca ctt atg ttc tca     2283
Lys Asp Trp Trp Ile Trp Gly Tyr Trp Thr Ser Pro Leu Met Phe Ser
            705                 710                 715

gtg aat gca atc ctt gtg aat gaa ttt gac gga aaa aag tgg aaa cat     2331
Val Asn Ala Ile Leu Val Asn Glu Phe Asp Gly Lys Lys Trp Lys His
        720                 725                 730

att gcg cca aat gga act gag ccg ctt gga cct gca gtg gta aga tct     2379
Ile Ala Pro Asn Gly Thr Glu Pro Leu Gly Pro Ala Val Val Arg Ser
    735                 740                 745

caa ggg ttc ttt ccc gat gca tat tgg tac tgg ata ggt gta ggt gca     2427
Gln Gly Phe Phe Pro Asp Ala Tyr Trp Tyr Trp Ile Gly Val Gly Ala
750                 755                 760                 765
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ctt gtt gga ttc aca gtt ctg ttt aac ata gcc tac agt ctt gct ctc     2475
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                770                 775                 780

gct tat ctt aac cca ttc gga aag cca caa gct aca att tca gaa gaa     2523
Ala Tyr Leu Asn Pro Phe Gly Lys Pro Gln Ala Thr Ile Ser Glu Glu
            785                 790                 795

agt gag agc aac gaa aat agt gaa tta tca acc cca ata gct agt aca     2571
Ser Glu Ser Asn Glu Asn Ser Glu Leu Ser Thr Pro Ile Ala Ser Thr
        800                 805                 810

acg gaa gga gat tct gtc ggt gag aat cag aat aag aaa gga atg gtt     2619
Thr Glu Gly Asp Ser Val Gly Glu Asn Gln Asn Lys Lys Gly Met Val
    815                 820                 825

ctt cca ttt gaa ccc cat tcc atc acc ttt gat gaa gtt gta tac tca     2667
Leu Pro Phe Glu Pro His Ser Ile Thr Phe Asp Glu Val Val Tyr Ser
830                 835                 840                 845

gtt gac atg cct ccg gaa atg aga gag caa ggt acc agt gac aat aga     2715
Val Asp Met Pro Pro Glu Met Arg Glu Gln Gly Thr Ser Asp Asn Arg
                850                 855                 860

ttg gta ctt ttg aag agt gtg agt gga gct ttc agg cca ggt gtt ctc     2763
Leu Val Leu Leu Lys Ser Val Ser Gly Ala Phe Arg Pro Gly Val Leu
            865                 870                 875

aca gct ctg atg gga gtt agt gga gcc ggt aaa aca aca ttg atg gat     2811
Thr Ala Leu Met Gly Val Ser Gly Ala Gly Lys Thr Thr Leu Met Asp
        880                 885                 890

gtc tta gct gga agg aaa act gga ggt tac att gac gga agc att aac     2859
Val Leu Ala Gly Arg Lys Thr Gly Gly Tyr Ile Asp Gly Ser Ile Asn
    895                 900                 905

att tct gga tat ccc aag aag caa gaa aca ttt gca cgt att tct gga     2907
Ile Ser Gly Tyr Pro Lys Lys Gln Glu Thr Phe Ala Arg Ile Ser Gly
910                 915                 920                 925

tac tgt gaa caa aac gac atc cat tca cct tat gta aca gtt tat gag     2955
Tyr Cys Glu Gln Asn Asp Ile His Ser Pro Tyr Val Thr Val Tyr Glu
                930                 935                 940

tcc ttg gtt tac tcg gct tgg ctg cgt tta cct caa gac gtt gat gag     3003
Ser Leu Val Tyr Ser Ala Trp Leu Arg Leu Pro Gln Asp Val Asp Glu
            945                 950                 955

aaa aag cga atg atg ttc gtt gaa caa gtt atg gaa ctt gtg gag ctt     3051
Lys Lys Arg Met Met Phe Val Glu Gln Val Met Glu Leu Val Glu Leu
        960                 965                 970

aca cca cta aga tct gcc tta gtc ggg ttg cca gga gtt aat ggt ctg     3099
Thr Pro Leu Arg Ser Ala Leu Val Gly Leu Pro Gly Val Asn Gly Leu
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acg att gca gtt gaa cta gta gca aac ccc tct  atc att ttt atg gac    3147
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990                 995                 1000                1005

gaa cca act tca gga  ttg gat gca aga gct  gct gca att gtg atg       3192
Glu Pro Thr Ser Gly  Leu Asp Ala Arg Ala  Ala Ala Ile Val Met
                1010                1015                1020

aga gct gtt agg aac  act gtc gat aca ggg  aga act gtt gtt tgt       3237
Arg Ala Val Arg Asn  Thr Val Asp Thr Gly  Arg Thr Val Val Cys
                1025                1030                1035

acc att cat cag cct  agc att gac att ttt  gag gcg ttc gat gag       3282
Thr Ile His Gln Pro  Ser Ile Asp Ile Phe  Glu Ala Phe Asp Glu
                1040                1045                1050

tta ttt ctt atg aaa  cga gga gga caa gag  ata tac gtc ggt cca       3327
Leu Phe Leu Met Lys  Arg Gly Gly Gln Glu  Ile Tyr Val Gly Pro
                1055                1060                1065

tta ggt cgt gag tca  agc cat ttg ata aag  tat ttt gag tct ata       3372
Leu Gly Arg Glu Ser  Ser His Leu Ile Lys  Tyr Phe Glu Ser Ile
                1070                1075                1080

ccc ggt gta acc aaa  ata aag gag ggg tac  aat cca gca act tgg       3417
Pro Gly Val Thr Lys  Ile Lys Glu Gly Tyr  Asn Pro Ala Thr Trp
                1085                1090                1095

atg tta gaa gtc aca  tct tcg tct caa gaa  ata aca tta ggt gtt       3462
Met Leu Glu Val Thr  Ser Ser Ser Gln Glu  Ile Thr Leu Gly Val
                1100                1105                1110

gat ttt acc gaa tta  tac aag aac tca gac  ctc ttc cgg agg aac       3507
Asp Phe Thr Glu Leu  Tyr Lys Asn Ser Asp  Leu Phe Arg Arg Asn
                1115                1120                1125

aaa gct ttg atc gag  gaa cta agt gtg cca  cgc cct ggt aca agt       3552
Lys Ala Leu Ile Glu  Glu Leu Ser Val Pro  Arg Pro Gly Thr Ser
                1130                1135                1140

gac ctg cat ttt gaa  act gaa ttc tca cag  cca ttt tgg gtc caa       3597
Asp Leu His Phe Glu  Thr Glu Phe Ser Gln  Pro Phe Trp Val Gln
                1145                1150                1155

tgt atg gct tgt ttg  tgg aag caa cac tgg  tca tac tgg cgt aat       3642
Cys Met Ala Cys Leu  Trp Lys Gln His Trp  Ser Tyr Trp Arg Asn
                1160                1165                1170

ccg gct tat act gca  gtc aga ttt ctc ttc  aca acc ttc ata gct       3687
Pro Ala Tyr Thr Ala  Val Arg Phe Leu Phe  Thr Thr Phe Ile Ala
                1175                1180                1185

ctc ata ttc ggg tca  atg ttc tgg gat att  ggt aca aaa gtg agt       3732
Leu Ile Phe Gly Ser  Met Phe Trp Asp Ile  Gly Thr Lys Val Ser
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ggg ccc caa gat ctg  aaa aac gcc atg gga  tct atg tat gct gct       3777
Gly Pro Gln Asp Leu  Lys Asn Ala Met Gly  Ser Met Tyr Ala Ala
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gtc ctc ttc ctt ggt  gtg cag aat tca tcg  tca gtt cag ccc gtt       3822
Val Leu Phe Leu Gly  Val Gln Asn Ser Ser  Ser Val Gln Pro Val
                1220                1225                1230

gta tct gtc gaa cgt  act gta ttt tac aga  gaa aaa gct gct gga       3867
Val Ser Val Glu Arg  Thr Val Phe Tyr Arg  Glu Lys Ala Ala Gly
                1235                1240                1245

atg tac tcc gcg atg  ccc tat gcc ttt gca  caa gtt ttc atc gaa       3912
Met Tyr Ser Ala Met  Pro Tyr Ala Phe Ala  Gln Val Phe Ile Glu
                1250                1255                1260

att cct tat gta ttt  gta caa gct gtt gtc  tat ggt ctc att gtc       3957
Ile Pro Tyr Val Phe  Val Gln Ala Val Val  Tyr Gly Leu Ile Val
                1265                1270                1275

tat tct atg att gga  ttt gaa tgg act gct  gca aaa ttc ttt tgg       4002
Tyr Ser Met Ile Gly  Phe Glu Trp Thr Ala  Ala Lys Phe Phe Trp
                1280                1285                1290

tac ttc ttc ttc atg  ttc ttc acc ttc ctc  tac ttc acc ttc ttt       4047
Tyr Phe Phe Phe Met  Phe Phe Thr Phe Leu  Tyr Phe Thr Phe Phe
                1295                1300                1305

ggc atg atg acc gtg  gct gtt acc ccg aac  caa aat gtt gct tca       4092
Gly Met Met Thr Val  Ala Val Thr Pro Asn  Gln Asn Val Ala Ser
                1310                1315                1320

atc gtt gcc gga ttc  ttc tat aca gta tgg  aat ctc ttc tca gga       4137
Ile Val Ala Gly Phe  Phe Tyr Thr Val Trp  Asn Leu Phe Ser Gly
                1325                1330                1335

ttc atc gtt cca cga  cct cgt att ccg ata  tgg tgg aga tgg tac       4182
Phe Ile Val Pro Arg  Pro Arg Ile Pro Ile  Trp Trp Arg Trp Tyr
                1340                1345                1350

tac tgg gct tgc cct  gtt gca tgg aca ttg  tat ggt ttg gtt gca       4227
Tyr Trp Ala Cys Pro  Val Ala Trp Thr Leu  Tyr Gly Leu Val Ala
                1355                1360                1365

tct caa ttt gga gac  ctc caa gat aca att  aat gat caa act gtg       4272
Ser Gln Phe Gly Asp  Leu Gln Asp Thr Ile  Asn Asp Gln Thr Val
                1370                1375                1380

gaa gat ttc ttg aga  agt agc tat gga ttt  aag cat gat ttt cta       4317
Glu Asp Phe Leu Arg  Ser Ser Tyr Gly Phe  Lys His Asp Phe Leu
                1385                1390                1395

gga gtt gtt gca gct  gtg atc gtt gca ttt  gca gtt gtt ttc gcc       4362
Gly Val Val Ala Ala  Val Ile Val Ala Phe  Ala Val Val Phe Ala
                1400                1405                1410
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ttc aca ttt gct ttg  ggt atc aag gca ttc  aat ttc cag aga aga       4407
Phe Thr Phe Ala Leu  Gly Ile Lys Ala Phe  Asn Phe Gln Arg Arg
                1415                1420                1425

tagaaatagt atttatttgt attcccagtt gttcatatat tcttgaataa gcttatgaag   4467

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Asn Gly Val Glu Ile Phe Ser Arg Ser Thr Arg Asp Glu Asp Asp Glu
        35                  40                  45

Glu Ala Leu Lys Trp Ala Ala Leu Glu Lys Leu Pro Thr Tyr Asp Arg
    50                  55                  60

Leu Arg Lys Gly Ile Leu Phe Gly Ser Gln Gly Thr Gly Val Ala Glu
65                  70                  75                  80

Val Asp Val Asp Asp Leu Gly Val Gln Gln Arg Lys Asn Leu Leu Asp
                85                  90                  95

Arg Leu Val Lys Ile Ala Glu Glu Asp Asn Glu Lys Phe Leu Leu Lys
            100                 105                 110

Leu Lys Asn Arg Ile Asp Arg Val Gly Ile Asp Phe Pro Ser Ile Glu
        115                 120                 125

Val Arg Phe Glu His Leu Asn Ile Glu Ala Asp Ala Tyr Val Gly Ser
    130                 135                 140

Arg Ala Leu Pro Thr Phe Thr Asn Phe Ile Ser Asn Phe Ile Glu Ser
145                 150                 155                 160
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Leu Leu Asp Ser Leu His Ile Leu Pro Ser Lys Lys Arg Ser Val Thr
165 170 175

Ile Leu Lys Asp Val Ser Gly Ile Val Lys Pro Cys Arg Met Thr Leu
180 185 190

Leu Leu Gly Pro Pro Gly Ser Gly Lys Thr Thr Leu Leu Leu Ala Leu
195 200 205

Ala Gly Lys Leu Asp Ser Ala Leu Arg Val Thr Gly Lys Val Thr Tyr
210 215 220

Asn Gly His Glu Leu His Glu Phe Val Pro Gln Arg Thr Ala Ala Tyr
225 230 235 240

Ile Ser Gln His Asp Leu His Ile Gly Glu Met Thr Val Arg Glu Thr
245 250 255

Leu Glu Phe Ser Ala Arg Cys Gln Gly Val Gly Ser Arg Tyr Glu Met
260 265 270

Leu Ala Glu Leu Ser Arg Arg Glu Lys Ala Ala Asn Ile Lys Pro Asp
275 280 285

Ala Asp Ile Asp Met Phe Met Lys Ala Ala Ser Thr Glu Gly Gln Glu
290 295 300

Ala Lys Val Ile Thr Asp Tyr Val Leu Lys Ile Leu Gly Leu Asp Ile
305 310 315 320

Cys Ala Asp Thr Met Val Gly Asp Gln Met Ile Arg Gly Ile Ser Gly
325 330 335

Gly Gln Lys Lys Arg Val Thr Thr Gly Glu Met Ile Val Gly Pro Ser
340 345 350

Lys Ala Leu Phe Met Asp Glu Ile Ser Thr Gly Leu Asp Ser Ser Thr
355 360 365

Thr Tyr Ser Ile Val Asn Ser Leu Lys Gln Ser Val Gln Ile Leu Lys
370 375 380

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Gly Thr Ala Leu Ile Ser Leu Leu Gln Pro Ala Pro Glu Thr Tyr Asn
385                 390                 395                 400

Leu Phe Asp Asp Ile Val Leu Leu Ser Asp Gly Tyr Ile Val Tyr Gln
                405                 410                 415

Gly Pro Arg Glu Glu Val Leu Asp Phe Phe Glu Ser Met Gly Phe Lys
            420                 425                 430

Cys Pro Asn Arg Lys Gly Val Ala Asp Phe Leu Gln Glu Val Thr Ser
        435                 440                 445

Lys Lys Asp Gln Gln Gln Tyr Trp Val Lys Arg Asp Glu Pro Tyr Arg
    450                 455                 460

Phe Ile Thr Ser Lys Glu Phe Ala Glu Ala Tyr Gln Ser Phe His Val
465                 470                 475                 480

Gly Arg Lys Val Ser Asp Glu Leu Thr Thr Ala Phe Asp Lys Ser Lys
                485                 490                 495

Ser His Pro Ala Ala Leu Thr Thr Glu Lys Tyr Gly Ile Gly Val Lys
            500                 505                 510

Gln Leu Leu Lys Val Cys Thr Glu Arg Glu Phe Leu Leu Met Gln Arg
        515                 520                 525

Asn Ser Phe Val Tyr Ile Phe Lys Phe Phe Gln Leu Met Val Ile Ala
    530                 535                 540

Leu Met Thr Met Thr Ile Phe Phe Arg Thr Lys Met Ser Arg Asp Thr
545                 550                 555                 560

Glu Thr Asp Gly Gly Ile Tyr Ser Gly Ala Leu Phe Phe Thr Val Val
                565                 570                 575

Met Leu Met Phe Asn Gly Leu Ser Glu Leu Pro Leu Thr Leu Tyr Lys
            580                 585                 590

Leu Pro Val Phe Tyr Lys Gln Arg Asp Phe Leu Phe Tyr Pro Ser Trp
        595                 600                 605
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Ala Tyr Ala Val Pro Ser Trp Ile Leu Lys Ile Pro Val Thr Phe Leu
610 615 620

Glu Val Gly Met Trp Val Phe Leu Thr Tyr Tyr Val Ile Gly Phe Asp
625 630 635 640

Pro Asn Val Gly Arg Phe Phe Lys Gln Phe Leu Leu Leu Ile Val Val
645 650 655

Asn Gln Met Ala Ser Gly Leu Phe Arg Phe Ile Ala Ala Val Gly Arg
660 665 670

Thr Met Gly Val Ala Ser Thr Phe Gly Ala Phe Ala Leu Leu Leu Gln
675 680 685

Phe Ala Leu Gly Gly Phe Val Leu Ala Arg Thr Asp Val Lys Asp Trp
690 695 700

Trp Ile Trp Gly Tyr Trp Thr Ser Pro Leu Met Phe Ser Val Asn Ala
705 710 715 720

Ile Leu Val Asn Glu Phe Asp Gly Lys Lys Trp Lys His Ile Ala Pro
725 730 735

Asn Gly Thr Glu Pro Leu Gly Pro Ala Val Val Arg Ser Gln Gly Phe
740 745 750

Phe Pro Asp Ala Tyr Trp Tyr Trp Ile Gly Val Gly Ala Leu Val Gly
755 760 765

Phe Thr Val Leu Phe Asn Ile Ala Tyr Ser Leu Ala Leu Ala Tyr Leu
770 775 780

Asn Pro Phe Gly Lys Pro Gln Ala Thr Ile Ser Glu Glu Ser Glu Ser
785 790 795 800

Asn Glu Asn Ser Glu Leu Ser Thr Pro Ile Ala Ser Thr Thr Glu Gly
805 810 815

Asp Ser Val Gly Glu Asn Gln Asn Lys Lys Gly Met Val Leu Pro Phe
820 825 830

Glu Pro His Ser Ile Thr Phe Asp Glu Val Val Tyr Ser Val Asp Met
835 840 845

Pro Pro Glu Met Arg Glu Gln Gly Thr Ser Asp Asn Arg Leu Val Leu
850 855 860

Leu Lys Ser Val Ser Gly Ala Phe Arg Pro Gly Val Leu Thr Ala Leu
865 870 875 880

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<301> Matsuoka and Nakamura
<302> Propeptide of a precursor to a plant vacuolar protein required for vacuolar targeting
<303> Proc. Natl. Acad. Sci. USA
<304> 88
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<307> 1991-02-01
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<301> Neuhaus, J.M.; Sticher, L.; Meins, F. and Boller, T.
<302> A short C-terminal sequence is necessary and sufficient for the targeting of chitinases to the plant vacuole
<303> Proc. Natl. Acad. Sci. USA
<304> 88
<305> 22
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<307> 1991-11-15

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